

Query= SEQ ID NO:6
(1458 letters)

Sequences producing significant alignments:

Score E
(bits) Value

AP003071.2.1.192759

474 e-131

>AP003071.2.1.192759
Length = 192759

Score = 474 bits (239), Expect = e-131
Identities = 245/247 (99%)
Strand = Plus / Plus

Query: 1 atgagctcagcctgctgggaggccacagggagatgcaggctgggcgggcggtggatggtt 60
|||||
Sbjct: 81847 atgagctcagcctgctgggaggccacagggagatgcaggctgggcgggcggtggatggtt 81906

Query: 61 ccaaccgggtgggtccggggcctggagctcagcctgtggggtggggacccagtgggtgccc 120
||| |||||
Sbjct: 81907 ccagccgggtgggtccggggcctggagctcagcctgtggggtggggacccagtgggtgccc 81966

Query: 121 tggagctgccgcttctgctctcagcaggatgatgggcaggacagggagaggctgacctac 180
|||||
Sbjct: 81967 tggagctgccgcttctgctcttagcaggatgatgggcaggacagggagaggctgacctac 82026

Query: 181 ttccagaacctgcctgagtccttgacttcctcctgggtgctgctgaccacggccaacaac 240
|||||
Sbjct: 82027 ttccagaacctgcctgagtccttgacttcctcctgggtgctgctgaccacggccaacaac 82086

Query: 241 cccgatg 247
|||||
Sbjct: 82087 cccgatg 82093

Score = 252 bits (127), Expect = 5e-64
Identities = 130/131 (99%)
Strand = Plus / Plus

Query: 659 gattctcaactgcgtcttcattgtgtactacctgttgagattgctgctcaaggtccttgc 718
|||||
Sbjct: 93396 gattctcaactgcgtcttcattgtgtactacctgttgagattgctgctcaaggtccttgc 93455

Query: 719 cctgggcctgcgaggggtacctgtcctaccccagcaacgtgtttgacgggctcctcacgt 778
|||||
Sbjct: 93456 cctgggcctgcgaggggtacctgtcctaccccagcaacgtgtttgacgggctcctcacgt 93515

Query: 779 tgtcctgctgg 789
 |||||||
Sbjct: 93516 tgtcctgctgg 93526

Score = 244 bits (123), Expect = 1e-61
Identities = 123/123 (100%)
Strand = Plus / Plus

Query: 480 caccgcccaggcccgagtaccagttctccgtttctgcagagcgcccagttcctcttcggc 539
 |||||||
Sbjct: 92987 caccgcccaggcccgagtaccagttctccgtttctgcagagcgcccagttcctcttcggc 93046

Query: 540 cactactactttgactacctggggaacctcatcgccctggcaaacctgggtgtccatttgc 599
 |||||||
Sbjct: 93047 cactactactttgactacctggggaacctcatcgccctggcaaacctgggtgtccatttgc 93106

Query: 600 gtg 602
 |||
Sbjct: 93107 gtg 93109

Score = 202 bits (102), Expect = 4e-49
Identities = 102/102 (100%)
Strand = Plus / Plus

Query: 378 gaaatctctccagacctcgctgtttcggaggcggctgggaacccgggctgcctttgaagt 437
 |||||||
Sbjct: 86414 gaaatctctccagacctcgctgtttcggaggcggctgggaacccgggctgcctttgaagt 86473

Query: 438 cctatcctccatggtgggggaggaggagccttcctcaggc 479
 |||||||
Sbjct: 86474 cctatcctccatggtgggggaggaggagccttcctcaggc 86515

Score = 200 bits (101), Expect = 2e-48
Identities = 101/101 (100%)
Strand = Plus / Plus

Query: 788 ggaggccggagatggtgggcctgctgtcgctgtgggacatgacctgcatgctgaacatgc 847
 |||||||
Sbjct: 95904 ggaggccggagatggtgggcctgctgtcgctgtgggacatgacctgcatgctgaacatgc 95963

Query: 848 tcatcgtgttcgcttcctgcgtatcatccccagcatgaag 888
 |||||||
Sbjct: 95964 tcatcgtgttcgcttcctgcgtatcatccccagcatgaag 96004

Score = 194 bits (98), Expect = 1e-46
Identities = 98/98 (100%)
Strand = Plus / Plus

Query: 1283 agaacttccttcacaagtgggacccccgcagccacctgcagccccttgctgggacccag 1342
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 101615 agaacttccttcacaagtgggacccccgcagccacctgcagccccttgctgggacccag 101674

Query: 1343 aggccacctaccagatgactgtggagctcctgttcagg 1380
 ||||||||||||||||||||||||||||
Sbjct: 101675 aggccacctaccagatgactgtggagctcctgttcagg 101712

Score = 172 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Plus

Query: 1119 ggctgccctggtcactctgtggaacttgatggtggtgaacaactggcaggtgtttctgga 1178
 ||||||||||||||||||||||||||||||||||||
Sbjct: 100341 ggctgccctggtcactctgtggaacttgatggtggtgaacaactggcaggtgtttctgga 100400

Query: 1179 tgcatatcggcgctactcaggcccggtg 1205
 ||||||||||||||||||||
Sbjct: 100401 tgcatatcggcgctactcaggcccggtg 100427

Score = 170 bits (86), Expect = 2e-39
Identities = 86/86 (100%)
Strand = Plus / Plus

Query: 1035 cagcctggccccctgccaatggctcggcgccctgtgggagcttcgagcagctggagtactg 1094
 ||||||||||||||||||||||||||||||||||||
Sbjct: 100173 cagcctggccccctgccaatggctcggcgccctgtgggagcttcgagcagctggagtactg 100232

Query: 1095 ggccaacaacttcgatgactttgcgg 1120
 ||||||||||||||||
Sbjct: 100233 ggccaacaacttcgatgactttgcgg 100258

Score = 163 bits (82), Expect = 4e-37
Identities = 82/82 (100%)
Strand = Plus / Plus

Query: 1377 cagggatattctggaggagccccggggaggatgagctcacagagaggctgagccagcaccc 1436
 ||||||||||||||||||||||||||||||||||||
Sbjct: 102377 cagggatattctggaggagccccggggaggatgagctcacagagaggctgagccagcaccc 102436

Query: 1437 gcacctgtggctgtgcaggtga 1458
|||||||
Sbjct: 102437 gcacctgtggctgtgcaggtga 102458

Score = 163 bits (82), Expect = 4e-37
Identities = 82/82 (100%)
Strand = Plus / Plus

Query: 1203 gtgggtccaagatctatTTTgtattgtgggtggctgggtgctgctgtcatctgggtcaacct 1262
|||||||
Sbjct: 101028 gtgggtccaagatctatTTTgtattgtgggtggctgggtgctgctgtcatctgggtcaacct 101087

Query: 1263 gtttctggccctgattctggag 1284
|||||||
Sbjct: 101088 gtttctggccctgattctggag 101109

Score = 155 bits (78), Expect = 9e-35
Identities = 78/78 (100%)
Strand = Plus / Plus

Query: 960 ggtggtctactacgtatTTTgccatcattgggatcaacttgTTtagaggcgctcattgtggc 1019
|||||||
Sbjct: 99714 ggtggtctactacgtatTTTgccatcattgggatcaacttgTTtagaggcgctcattgtggc 99773

Query: 1020 tcttcctggaaacagcag 1037
|||||||
Sbjct: 99774 tcttcctggaaacagcag 99791

Score = 145 bits (73), Expect = 9e-32
Identities = 73/73 (100%)
Strand = Plus / Plus

Query: 891 gatggccgtggtggccagtaccgtcctgggcctgggtgcagaacatgcgtgcgtttggcgg 950
|||||||
Sbjct: 98452 gatggccgtggtggccagtaccgtcctgggcctgggtgcagaacatgcgtgcgtttggcgg 98511

Query: 951 gatcctggtggtg 963
|||||||
Sbjct: 98512 gatcctggtggtg 98524

Score = 135 bits (68), Expect = 9e-29
Identities = 68/68 (100%)
Strand = Plus / Plus

Query: 247 gtgatgattcctgcgtattccaagaaccgggcctatgccatcttcttcacatagtccttcact 306
|||||
Sbjct: 84921 gtgatgattcctgcgtattccaagaaccgggcctatgccatcttcttcacatagtccttcact 84980

Query: 307 gtgatagg 314
|||||
Sbjct: 84981 gtgatagg 84988

Score = 133 bits (67), Expect = 3e-28
Identities = 67/67 (100%)
Strand = Plus / Plus

Query: 312 aggaagcctgtttctgatgaacctgctgacagccatcatctacagtcagttccggggcta 371
|||||
Sbjct: 85846 aggaagcctgtttctgatgaacctgctgacagccatcatctacagtcagttccggggcta 85905

Query: 372 cctgatg 378
|||||
Sbjct: 85906 cctgatg 85912

Score = 119 bits (60), Expect = 5e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

Query: 600 gtgttcctgggtgctggatgcagatgtgctgcctgctgagcgtgatgacttcacccctgggg 659
|||||
Sbjct: 93239 gtgttcctgggtgctggatgcagatgtgctgcctgctgagcgtgatgacttcacccctgggg 93298



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

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File

Get Subsequence

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☐ 1: AP003071. Homo sapiens geno...[gi:22202827]

Links

LOCUS AP003071 191898 bp DNA linear PRI 10-AUG-2002
 DEFINITION Homo sapiens genomic DNA, chromosome 11 clone:RP11-554A11, complete sequence.

ACCESSION AP003071

VERSION AP003071.3 GI:22202827

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens genomic DNA

JOURNAL Published Only in Database (2001)

REFERENCE 2 (bases 1 to 191898)

 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

 JOURNAL Submitted (28-DEC-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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COMMENT On Aug 9, 2002 this sequence version replaced gi:21327964.

FEATURES

source

Location/Qualifiers

1..191898

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q"

/clone="RP11-554A11"

BASE COUNT 41232 a 49917 c 52993 g 47756 t

ORIGIN

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61 gtcttttgtc ttgcttaact tctgaaaaga ggtctgtaat aattctcatc cttttctctc
121 tgtctttttt tttttttttt gatacagggt ctggctctgt caccagggtt ggaatgcagt
181 ggcattgatt cgactcactg caatcttcat ctctggggtt caagccatcc tcccacctca
241 gcctcccatg tagctgggac tacagggtgca tgccaccatg cccgggctaat ttttgtattt
301 tttgtagaga tggaattca ccatgttgcc caggctgggt tcaaaactcgt gagctcaagc
361 aatccaccta ccacagcctc ccaaagtgtt gggattacag gcatgagcca ctgcacctgg
421 ccattctctg ctgtttttta ggtcttctct ttatcattgg ttttcaaaag tgtagatatg
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